REMARKS

After entry of this amendment, claims 1-11, 15, 17, 25 and 27-32 are pending, of which claims 1-10, 24-25 and 29-30 are withdrawn. Claim 16 has been cancelled without prejudice or disclaimer. Claims 11, 31 and 32 have been amended without prejudice or disclaimer and find support *inter alia* in the original claims. Claim 11 as amended finds further support in the specification at page 26, lines 11-16, and page 40, lines 37-43. No new matter has been added.

Withdrawn claims have also been amended to require all the limitations of the product claims. Support is found *inter alia* in the original claims. Claim 1 finds further support in the specification at page 26, lines 11-16, and page 40, lines 37-43. No new matter has been added. Should the claims be found allowable, the withdrawn claims which depend from or otherwise include all the limitations of an allowable claim are requested to be rejoined. See MPEP § 821.04.

Upon review of the specification, Applicants noted that the sequences listed on Table 10 at page 92 of the specification were incorrectly entered into the Sequence Listing submitted with First preliminary Amendment dated September 30, 2005. Consequently, the sequence identifier numbers were incorrectly assigned to those sequences. Accordingly, Applicants submit herewith a revised Sequence Listing which conforms to 37 CFR §§ 1.821-1.825 *via* EFS-Web, and a Statement to Support Filing and Submission in Accordance with 37 CFR §§ 1.821-1.825. The errors found in the Sequence Listing previously submitted have been corrected. Support for the amendments made to the Sequence Listing is found in the Sequence Listing as originally filed and in the specification at page 92, line 1, and Table 10. The corresponding sequence identifier numbers (SEQ ID NO) have also been added to the primer sequences listed on Table 10 at page 92 of the specification. Furthermore, the specification has been amended to include a paragraph directed to the incorporation of the sequence listing submitted herewith *via* EFS-Web. No new matter has been added to the Sequence Listing or the specification. Entry of this Sequence Listing into the application is requested.

Additionally, in preparing the present response, Applicants discovered that the clone No. referring to in Example 16 at page 96, line 24, *i.e.* MaLPAAT2.1, was incorrect, which is an inadvertent mistake by Applicants. As referring to in Example 16, the primers MaLPAAT2.1 are

"stated." However, the only primers stated in the specification for MaLPAAT are MaLPAAT1.1 and MaLPAAT1.2 in Table 10 at page 92. Thus, the correct clone No. should be "MaLPAAT1.1" as now amended. It is respectfully submitted that the mistake made in the specification is an obvious typographic error that one skilled in the art would recognize. An amendment to correct such an obvious error does not constitute new matter. See *In re Oda*, 443 F.2d 1200 (CCPA 1971); see also MPEP § 2163.07. Entry of the amendment to the specification to correct this inadvertent mistake is respectfully requested.

Claim Rejection – 35 USC § 112

Claims 11, 15, 17-23, 27, 28, 31 and 32 are rejected under 35 U.S.C. § 112, first paragraph, for allegedly failing to comply with the written description requirement and lack of an enabling disclosure. Applicants respectfully disagree. However, to expedite prosecution, claim 11 has been amended without prejudice or disclaimer to recite the nucleotide sequence with more specificity. Applicants respectfully request reconsideration in light of the present amendment and for the following reasons.

Written Description

The rejection states that the specification describes only the sequence of SEQ ID NO: 16 encoding SEQ ID NO: 17, but not other sequences within the claimed genus. The Examiner further alleges that the specification fails to disclose any particular features that confer the claimed functional activity. Applicants respectfully disagree that the claims as amended are not described.

As amended, claim 11 specifies the nucleotide sequence to be the sequence of SEQ ID NO: 16, a nucleotide sequence encoding the polypeptide sequence of SEQ ID NO: 17, or a nucleotide sequence having at least 95% identity with the sequence of SEQ ID NO: 16 or encoding a polypeptide sequence having at least 95% identity with SEQ ID NO: 17. It is respectfully submitted that the specification provides sufficient written description for the claimed genus as defined by the amended claim.

As noted by the Examiner, the specification describes the sequence of SEQ ID NO: 16 that encodes SEQ ID NO: 17. Knowledge of the genetic code and its redundancies and the disclosure of SEQ ID NO: 17, when combined with the pre-existing knowledge in the art, would

have put the skilled artisan in possession of the genus of nucleic acids that encodes SEQ ID NO: 17. With the aid of a computer, one skilled in the art could easily envision all of the nucleic acids that encode a polypeptide with at least 95% identity with SEQ ID NO: 17. Furthermore, the methods for performing screening and testing the enzymatic activity of the polypeptide encoded by the isolated nucleic acid are described in the specification (see e.g., Example 16) and were routine and well known to those skilled in the art. Thus, one of ordinary skill in the art would conclude that Applicants were in possession of the claimed genus at the time the application was filed.

Furthermore, as described in the specification at page 46, lines 10-30, natural variations (e.g. DNA sequence polymorphisms) can lead to alterations in the amino acid sequences of the lysophosphatidic acid acyltransferase (LPAAT) within a population, bringing about a variation of 1-5% in the nucleotide sequence of the LPAAT gene without altering the functional activity of the LPAAT. Accordingly, the claim scope created by the recitation of at least 95% identity with SEQ ID NO: 16 includes the expected range of natural polymorphic variants, which Applicants should be permitted to claim such variations of the disclosed embodiment of the invention.

Moreover, as discussed in the Response dated April 22, 2008, the specification discloses numerous LPAATs, among which the second LPAAT coding sequence from Mortierella alpina is 100% identical to SEQ ID NO: 16 in the overlapping region. Thus, the specification provides at least two species that are within the genus recited in the claim as amended, and allows the skilled artisan to readily envision further species having the claimed level of identity. Because these two sequences clearly constitute a representative number of species within the claimed genus of sequences, it is respectfully submitted that the claims as amended satisfy the written description requirement.

For at least the above reasons, reconsideration and withdrawn of the rejection is respectfully requested.

Enablement

The Examiner alleges that the specification does not provide any evidence showing that SEQ ID NO: 16 encodes MaLPAAP and is the sequence that was used to transform yeast in Example 16. The Examiner further asserts that the specification does not provide conserved

residues and motifs that are required to retain the LPAAT activity. The Examiner concludes that undue experimentation would be required to practice the claimed invention. Applicants respectfully disagree.

As discussed in the Response dated April 22, 2008, Example 16 at pages 96-98 discloses expression of a Mortierella LPAAT (MaLPAAT) in yeast and the LPAAT enzymatic activity was confirmed by the feeding experiments with the transformed yeast as demonstrated in Figure 23-26. According to the description of Example 16, the "stated" primers MaLPAAT2.1 were used to amplify the MaLPAAT cDNA *via* PCR for subsequent cloning and transformation. See page 96, lines 24-31. However, as discussed above at pages 9-10 of this response, the only primers disclosed (and "stated") in the specification for MaLPAAT are MaLPAAT1.1 and MaLPAAT1.2 in Table 10 at page 92. Applicants submit that the term "MaLPAAT2.1" used in Example 16 is an obvious typographic error for "MaLPAAT1.1," which is the primer pair used for cloning the clone No. MaLPAAT1.1.

Furthermore, as described in Table 9 at page 91, the clone No. MaLPAAT1.1 is the acyltransferase obtained from M. alpina that shows homology with LPAAT. The sequences of the primer set for amplifying MaLPAAT1.1 is further provided in Table 10 at page 92. A sequence alignment between SEQ ID NO: 16 and the primer set designed for the clone No. MaLPAAT1.1 indicates that this primer set contains the 5'-end and the 3'-end primers that were designed to amplify the full-length of SEQ ID NO: 16. A copy of the sequence alignment is enclosed with this response for the Examiner's easy reference. Accordingly, it is respectfully submitted that one of ordinary skill in the art, when reading the specification, will reasonably infer that the sequence of SEQ ID NO: 16 corresponds to the clone No. MaLPAAT1.1, and thus, encodes a MaLPAAT.

Moreover, as discussed in the Response dated April 22, 2008, in addition to SEQ ID NO: 16, the specification further provides a second MaLPAAT coding sequence and LPAAT coding sequences from other species such as Thraustochytrium, Physcomitrella patens, and Shewanella hanedai. When aligning various LPAAT enzymes such as those disclosed in the instant specification, one of ordinary skill in the art would readily be able to identify conserved residues and motifs, and know where (and where not) to effect substitutions. Method of generating such mutations or substitutions, for example, site-directed mutagenesis and PCR-mediated

mutagenesis, are standard techniques readily available and known to those skilled in the art. See specification at page 48, lines 29-34. Furthermore, the screening and selecting of a nucleic acid with the specified sequence homology while maintaining the desired enzymatic property is routine to those skilled in the art and is described in the specification.

Additionally, the specification provides detailed guidance on how to isolate and clone LPAAT coding nucleic acid from various species (Example 13), how to determine the enzymatic activity of the polypeptide encoded by the isolated nucleic acid in straightforward assays (Example 16), how to generate transgenic organisms such as plants (Example 18), and how to analyze the transgenic plants (Example 19). It is submitted that determining the enzymatic activity is routine and not undue experimentation. As stated in *Ex parte Jackson*, under the applicable law, the test for "undue experimentation" is not merely quantitative, since a considerable amount of experimentation is permissible, if it is merely routine, or if the specification in question provides a reasonable amount of guidance with respect to the direction in which the experimentation should proceed to enable the determination of how to practice a desired embodiment of the invention claimed. *Ex parte Jackson*, 217 USPQ 804, 807 (1982). On the facts of this case, the detailed guidance provided in the specification and the routine nature of the screening and testing required for making and using the claimed invention weigh in favor of finding enablement.

Accordingly, in view of the detailed description, guidance, working examples, state and knowledge of the art, and high level of skill, the specification enables the claims without undue experimentation. On these facts, a proper analysis of the relevant factors supports enablement. *In re Wands*, 858 F.2d 731, 737 (Fed. Cir. 1988). Reconsideration and withdrawal of the enablement rejection is respectfully requested.

CONCLUSION

In view of the above remarks and further in view of the above amendments, Applicants respectfully request withdrawal of the rejections and allowance of the claims. If any outstanding issues remain, the Examiner is invited to telephone the undersigned at the number given below.

Applicants reserve all rights to pursue the non-elected claims and subject matter in one or more divisional applications, if necessary.

Accompanying this response is a petition for a two-month extension of time to and including January 13, 2009, to respond to the Office Action mailed August 13, 2008 with the required fee. No further fees are believed due. However, if a fee is due, please charge our Deposit Account No. 03-2775, under Order No. 13478-00002-US from which the undersigned is authorized to draw.

Respectfully submitted,

By /s/ Hui-Ju Wu

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Attachment: Sequence alignment between SEQ ID NO: 16 and MaLPAAT1.1 primer set

Sequence alignment between SEQ ID NO: 16 ("SIN:!") and the primer set MaLPAAT1.1, SEQ ID NO: 123 ("SIN:123") and the reverse compliment of SEQ ID NO: 124 ("SIN:124(R)").

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SIN:16      ATGGATGAATCCACCACGACCACCACGCACCACTCAGAGACCAGCAGCAAGACGTCCTCG 60
SIN:123     ATGGATGAATCCACCACGACCA

SIN:16      CACCCCCGCCGGCTCGGTCCCGAGATGAACCCTATCTACAAGGGTCTGCGAGCCATTGTC 120

SIN:16      TGGGCCTTTTACTTCAACCTGGGAGCGTCGCTTATATCGATCACGCAGGTGCTGTCGCTG 180

SIN:16      CCTCTGGCGTTGATTGCTCCAGGGGTCTACCAGTGGCACATCAGCAAAACACAGGGTCAC 240

SIN:16      TTTGGAGCTTTCCTGCTCCGGATGAACCAGCTCTTTGCGCCGTCAGATATTGTCTTGACA 300

SIN:16      GGGGACGAGAGTGTCAGGGGAATCGTCAAGGTCTACAAAGGACGGAACCTGAAGGAGGCC 360

SIN:16      GGTGAGCCAGGCAGCGGTCAGGGAGAGGACATTCTTCTGGATATGCCCGAGAGGATGGTT 420

SIN:16      TTCATTGCGAACCACCAGATCTACTCTGACTGGATGTACCTCTGGTGCTTCTCCTATTTT 480

SIN:16      GCAGAGAGGCACAGGGCACTGAAGATTATTCTTCGGGGCGACCTGACCTGGATCCCTGTC 540

SIN:16      TTTGGCTGGGGTATGCGGTTCTTTGACTTTATCTTTTTGAAACGTAATGACTGGGCACAC 600

SIN:16      GATCGCCGTGCCATTGAGGAAAACTTGGGACGTGTCAAGGAAAAGGATCCCCTCTGGCTC 660

SIN:16      GTGGTCTTCCCCGAGGGAACAGTCGTCTCCAAGGAAACGCGTCTCCGATCCGTTGCCTTT 720

SIN:16      TCAAAGAAGGCTAGTCTGTCGGATCACCGCCATGTGCTGCTTCCAAGGACCAGCGGTCTG 780

SIN:16      TTTGTGTGCATCAACAAGTTGCGTGGATCTGTCGACTACTTGTACGATGCAACCGTTGGC 840

SIN:16      TACTCGAATGTCGAGTATGGCGAGATTCCGCAGGAGCTTTACCCGTTACCAGGACTGTAT 900

SIN:16      ATCAACAAAGCACAGCCCAAGGAGATCAACATGCACCTGCGTCGATTTGCGATCAAGGAT 960

SIN:16      ATCCCCACGTCAGAACCCGAATTTGTGGAATGGGTCCGAGCTCGGTGGGTGGAGAAGGAT 1020

SIN:16      GAGTTGATGGAAGAGTTTTATACCAAGGGCCGATTTCCATCACAACTGACGGCCGCCGAC 1080

SIN:16      ATTGGTGAGAAGGAGGTCAAGACGGCAGGAGGTCCAACGGAGGGACAGAGTGTCAGGATC 1140

SIN:16      CCGCTCAAGGCGCGAGGCATGATGGACTACCTCATGCCCTCGGTCATGAATCTGATCGCC 1200

SIN:16      CTTCCTGTGCTGGCGTTTGCGATGAGATATGCAGTGCAGCAAGCATCGGGCTGA       1254
SIN:124(R)                                    GCAGCAAGCATCGGGCTGA
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